Appendix A

Gap Results SEQ ID NO: 1 vs. SEQ ID NO: 2

GAP of: SID 1 check: 418 from: 1 to: 476

WPDEF SVBV E3 Promoter fragment

 to: SID 2 check: 1650 from: 1 to: 518

WPDEF SVBV E3 Promoter

 Symbol comparison table: nwsgapdna.cmp CompCheck: 8760

Gap Weight:	50	Average Match:	10.000
Length Weight:	3	Average Mismatch:	0.000

Quality:	4760	Length:	518
Ratio:	10.000	Gaps:	0
Percent Similarity:	100.000	Percent Identity:	100.000

         Match display thresholds for the alignment(s):
                       | = IDENTITY
                       : =   5
                       . =   1

SID 1 x SID 2   October 12, 2004 11:44 ..

    1 ....aactatgctgatgacaagataattctaataagcaat 36
                   ||||||||||||||||||||||||||||||||||||
    1 ggatcccccagcttaactatgctgatgacaagataattctaataagcaat 50

   37 tattcagaattaatcaaggagaaagaattaataactctttcagaatatga 86
      ||||||||||||||||||||||||||||||||||||||||||||||||||
   51 tattcagaattaatcaaggagaaagaattaataactctttcagaatatga 100

   87 agcccgctttacaagtggccagctagctatcactgaaaagacagcaagac 136
      ||||||||||||||||||||||||||||||||||||||||||||||||||
  101 agcccgctttacaagtggccagctagctatcactgaaaagacagcaagac 150

  137 aatggtgtctcgatgcaccagaaccacatctttgcagcagatgtgaagca 186
      ||||||||||||||||||||||||||||||||||||||||||||||||||
  151 aatggtgtctcgatgcaccagaaccacatctttgcagcagatgtgaagca 200

  187 gccagagtggtccacaagacgcactcagaaaaggcatcttctaccgacac 236
      ||||||||||||||||||||||||||||||||||||||||||||||||||
  201 gccagagtggtccacaagacgcactcagaaaaggcatcttctaccgacac 250

  237 agaaaaagacaaccacagctcatcatccaacatgtagactgtcgttatgc 286
      ||||||||||||||||||||||||||||||||||||||||||||||||||
  251 agaaaaagacaaccacagctcatcatccaacatgtagactgtcgttatgc 300

  287 gtcggctgaagataagactgaccccaggccagcactaaagaagaaataat 336

```
    |||||||||||||||||||||||||||||||||||||||||||||||||
301 gtcggctgaagataagactgaccccaggccagcactaaagaagaaataat 350

337 gcaagtggtcctagctccactttagctttaataattatgtttcattatta 386
    ||||||||||||||||||||||||||||||||||||||||||||||||||
351 gcaagtggtcctagctccactttagctttaataattatgtttcattatta 400

387 ttctctgcttttgctctctatataaagagcttgtattttcatttgaaggc 436
    ||||||||||||||||||||||||||||||||||||||||||||||||||
401 ttctctgcttttgctctctatataaagagcttgtattttcatttgaaggc 450

437 agaggcgaacacacacacagaacctccctgcttacaaacc.......... 476
    ||||||||||||||||||||||||||||||||||||||||||
451 agaggcgaacacacacacagaacctccctgcttacaaaccggatcgggct 500
```

Gap Results SEQ ID NO: 1 vs. SEQ ID NO: 3

GAP of: SID 1 check: 418 from: 1 to: 476

WPDEF SVBV E3 Promoter fragment

 to: SID 3 check: 303 from: 1 to: 651

WPDEF seSVBV promoter
1-108 of SVBV replaced by 92-362 of SBVB

 Symbol comparison table: nwsgapdna.cmp CompCheck: 8760

```
        Gap Weight:      50      Average Match: 10.000
     Length Weight:       3   Average Mismatch:  0.000

           Quality:    3971             Length:    654
             Ratio:   8.342               Gaps:      1
Percent Similarity: 85.201   Percent Identity: 85.201
```

        Match display thresholds for the alignment(s):
                     | = IDENTITY
                     : = 5
                     . = 1

SID 1 x SID 3   October 12, 2004 11:45 ..

```
   1 ......................aactatgctgatgacaagataattcta 27
                              |  |   |  |  || |
 151 cagaaaaagacaaccacagctcatcatccaacatgtagactgtcgttatg 200

  28 ataagcaattattcagaattaatcaaggagaaagaattaataactctttc 77
        |      |    |  | | | | |   | | | | | || |     |
 201 cgtcggctgaagataagactgaccccaggccagcactaaagaagaaataa 250

  78 agaatatgaagcccgctttacaagtggccagctagctatcactgaaaaga 127
      | |  ||  |  ||| | | |     ||||||||||||||||||||||
 251 tgcaagtggtcctagct...ccactttagcgctagctatcactgaaaaga 297

 128 cagcaagacaatggtgtctcgatgcaccagaaccacatctttgcagcaga 177
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 298 cagcaagacaatggtgtctcgatgcaccagaaccacatctttgcagcaga 347

 178 tgtgaagcagccagagtggtccacaagacgcactcagaaaaggcatcttc 227
     |||||||||||||||||||||||||||||:|||||||||||||||||||||
 348 tgtgaagcagccagagtggtccacaagacgcactcagaaaaggcatcttc 397

 228 taccgacacagaaaaagacaaccacagctcatcatccaacatgtagactg 277
     |||||||||||||||||||||||||||||:||||||||||||||||||||
 398 taccgacacagaaaaagacaaccacagctcatcatccaacatgtagactg 447
```

```
278 tcgttatgcgtcggctgaagataagactgaccccaggccagcactaaaga 327
    ||||||||||||||||||||||||||||||||||||||||||||||||||
448 tcgttatgcgtcggctgaagataagactgaccccaggccagcactaaaga 497

328 agaaataatgcaagtggtcctagctccactttagctttaataattatgtt 377
    ||||||||||||||||||||||||||||||||||||||||||||||||||
498 agaaataatgcaagtggtcctagctccactttagctttaataattatgtt 547

378 tcattattattctctgcttttgctctctatataaagagcttgtattttca 427
    ||||||||||||||||||||||||||||||||||||||||||||||||||
548 tcattattattctctgcttttgctctctatataaagagcttgtattttca 597

428 tttgaaggcagaggcgaacacacacacagaacctccctgcttacaaacc. 476
    |||||||||||||||||||||||||||||||||||||||||||||||||
598 tttgaaggcagaggcgaacacacacacagaacctccctgcttacaaaccg 647
```

Gap Results SEQ ID NO: 1 vs. SEQ ID NO: 4

GAP of: SID 1 check: 418 from: 1 to: 476

WPDEF SVBV E3 Promoter fragment

 to: SID 4 check: 7979 from: 1 to: 701

WPDEF leSVBV
1-108 of SVBV replaced by 92-404 of SVBV

 Symbol comparison table: nwsgapdna.cmp CompCheck: 8760

        Gap Weight: 50   Average Match: 10.000
     Length Weight: 3   Average Mismatch: 0.000

         Quality: 4049   Length: 704
           Ratio: 8.506   Gaps: 2.
Percent Similarity: 88.161   Percent Identity: 88.161

        Match display thresholds for the alignment(s):
               | - IDENTITY
               : =   5
               . --   1

SID 1 x SID 4   October 12, 2004 11:46 ..


```
   1 ..........aactatgctgatgacaagataattctaataagcaattatt 40
              | |   |||| || ||| || |  || ||  ||  ||
 201 gtcggctgaagataagactgaccccaggccagcactaaagaagaaataat 250

  41 cagaattaatcaaggagaa....agaattaataactctttcagaatatga 86
      | |   | | ||      || |||||||| | |  | | || |
 251 gcaagtggtcctagctccactttagctttaataattatgtttcattatta 300

  87 agcccgctttacaagtggccagctagctatcactgaaaagacagcaagac 136
      | |   ||       |   ||||||||||||||||||||||||||||
 301 ttctctgctt...ttgctctcgctagctatcactgaaaagacagcaagac 347

 137 aatggtgtctcgatgcaccagaaccacatctttgcagcagatgtgaagca 186
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 348 aatggtgtctcgatgcaccagaaccacatctttgcagcagatgtgaagca 397

 187 gccagagtggtccacaagacgcactcagaaaaggcatcttctaccgacac 236
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 398 gccagagtggtccacaagacgcactcagaaaaggcatcttctaccgacac 447

 237 agaaaaagacaaccacagctcatcatccaacatgtagactgtcgttatgc 286
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 448 agaaaaagacaaccacagctcatcatccaacatgtagactgtcgttatgc 497
```

```
287 gtcggctgaagataagactgaccccaggccagcactaaagaagaaataat 336
    ||||||||||||||||||||||||||||||||||||||||||||||||||
498 gtcggctgaagataagactgaccccaggccagcactaaagaagaaataat 547

337 gcaagtggtcctagctccactttagctttaataattatgtttcattatta 386
    ||||||||||||||||||||||||||||||||||||||||||||||||||
548 gcaagtggtcctagctccactttagctttaataattatgtttcattatta 597

387 ttctctgcttttgctctctatataaagagcttgtattttcatttgaaggc 436
    ||||||||||||||||||||||||||||||||||||||||||||||||||
598 ttctctgcttttgctctctatataaagagcttgtattttcatttgaaggc 647

437 agaggcgaacacacacacagaacctccctgcttacaaacc.......... 476
    |||||||||||||||||||||||||||||||||||||||||
648 agaggcgaacacacacacagaacctccctgcttacaaaccggatcgggct 697
```

Multiple Sequence Alignment: SEQ ID NO: 1-4

Symbol comparison table: pileupdna.cmp CompCheck: 6876

```
                    GapWeight: 5
                GapLengthWeight: 1

  SID_1_pileup_405724.txt  MSF: 716  Type: N  October 8, 2004 12:10
Check: 6538 ..

Name: SID_1            Len:  476  Check: 2120  Weight:  1.00
Name: SID_2            Len:  518  Check: 8412  Weight:  1.00
Name: SID_3            Len:  651  Check: 1160  Weight:  1.00
Name: SID_4            Len:  701  Check: 4846  Weight:  1.00

//
          1                                                50
    SID_1  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
    SID_2  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
    SID_3  ggatccgctt tacaagtggc cacctagcta tcactgaaaa gacagcaaga
    SID_4  ~gatccgctt tacaagtggc cacctagcta tcactgaaaa gacagcaaga

          51                                               100
    SID_1  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
    SID_2  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
    SID_3  caatggtgtc tcgatgcacc agaaccacat ctttgcagca gatgtgaagc
    SID_4  caatggtgtc tcgatgcacc agaaccacat ctttgcagca gatgtgaagc

          101                                              150
    SID_1  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
    SID_2  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
    SID_3  agccagagtg gtccacaaga cgcactcaga aaaggcatct tctaccgaca
    SID_4  agccagagtg gtccacaaga cgcactcaga aaaggcatct tctaccgaca

          151                                              200
    SID_1  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
    SID_2  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~gga
    SID_3  cagaaaaaga caaccacagc tcatcatcca acatgtagac tgtcgttatg
    SID_4  cagaaaaaga caaccacagc tcatcatcca acatgtagac tgtcgttatg

          201                                              250
    SID_1  ~~~~~~~~~~ ~aactatgct gatgacaaga taattctaat aagcaattat
    SID_2  tcccccagct taactatgct gatgacaaga taattctaat aagcaattat
    SID_3  cgtcggctga agataagact gaccccaggc cagcactaaa gaagaaataa
    SID_4  cgtcggctga agataagact gaccccaggc cagcactaaa gaagaaataa

          251                                              300
    SID_1  tcagaattaa tcaaggagag agaattaata actctttcag aatatgaagc
    SID_2  tcagaattaa tcaaggagag agaattaata actctttcag aatatgaagc
    SID_3  tgcaagtggt cctagctcca ctttag.... .......... ..........
    SID_4  tgcaagtggt cctagctcca ctttagcttt aataattatg tttcattatt
```

```
      301                                                                   350
SID_1 ccgctttaca agtg.gccag ctagctatca ctgaaaagac agcaagacaa
SID_2 ccgctttaca agtg.gccag ctagctatca ctgaaaagac agcaagacaa
SID_3 .......... ........cg ctagctatca ctgaaaagac agcaagacaa
SID_4 attctctgct tttgctctcg ctagctatca ctgaaaagac agcaagacaa

      351                                                                   400
SID_1 tggtgtctcg atgcaccaga accacatctt tgcagcagat gtgaagcagc
SID_2 tggtgtctcg atgcaccaga accacatctt tgcagcagat gtgaagcagc
SID_3 tggtgtctcg atgcaccaga accacatctt tgcagcagat gtgaagcagc
SID_4 tggtgtctcg atgcaccaga accacatctt tgcagcagat gtgaagcagc

      401                                                                   450
SID_1 cagagtggtc cacaagacgc actcagaaaa ggcatcttct accgacacag
SID_2 cagagtggtc cacaagacgc actcagaaaa ggcatcttct accgacacag
SID_3 cagagtggtc cacaagacgc actcagaaaa ggcatcttct accgacacag
SID_4 cagagtggtc cacaagacgc actcagaaaa ggcatcttct accgacacag

      451                                                                   500
SID_1 aaaaagacaa ccacagctca tcatccaaca tgtagactgt cgttatgcgt
SID_2 aaaaagacaa ccacagctca tcatccaaca tgtagactgt cgttatgcgt
SID_3 aaaaagacaa ccacagctca tcatccaaca tgtagactgt cgttatgcgt
SID_4 aaaaagacaa ccacagctca tcatccaaca tgtagactgt cgttatgcgt

      501                                                                   550
SID_1 cggctgaaga taagactgac cccaggccag cactaaagaa gaaataatgc
SID_2 cggctgaaga taagactgac cccaggccag cactaaagaa gaaataatgc
SID_3 cggctgaaga taagactgac cccaggccag cactaaagaa gaaataatgc
SID_4 cggctgaaga taagactgac cccaggccag cactaaagaa gaaataatgc

      551                                                                   600
SID_1 aagtggtcct agctccactt tagctttaat aattatgttt cattattatt
SID_2 aagtggtcct agctccactt tagctttaat aattatgttt cattattatt
SID_3 aagtggtcct agctccactt tagctttaat aattatgttt cattattatt
SID_4 aagtggtcct agctccactt tagctttaat aattatgttt cattattatt

      601                                                                   650
SID_1 ctctgctttt gctctctata taaagagctt gtattttcat ttgaaggcag
SID_2 ctctgctttt gctctctata taaagagctt gtattttcat ttgaaggcag
SID_3 ctctgctttt gctctctata taaagagctt gtattttcat ttgaaggcag
SID_4 ctctgctttt gctctctata taaagagctt gtattttcat ttgaaggcag

      651                                                                   700
SID_1 aggcgaacac acacacagaa cctccctgct tacaaacc~~ ~~~~~~~~~~
SID_2 aggcgaacac acacacagaa cctccctgct tacaaaccgg atcgggctgc
SID_3 aggcgaacac acacacagaa cctccctgct tacaaaccgg atc~~~~~~~
SID_4 aggcgaacac acacacagaa cctccctgct tacaaaccgg atcgggctgc

      701                      716
SID_1 ~~~~~~~~~~ ~~~~~~
SID_2 aggtctctaa ccatgg
SID_3 ~~~~~~~~~~ ~~~~~~
SID_4 ag~~~~~~~~ ~~~~~~
```